**BLASTP 2.2.6 [Apr-09-2003]**

RID: 1067455426-9658-2307585.BLASTQ3

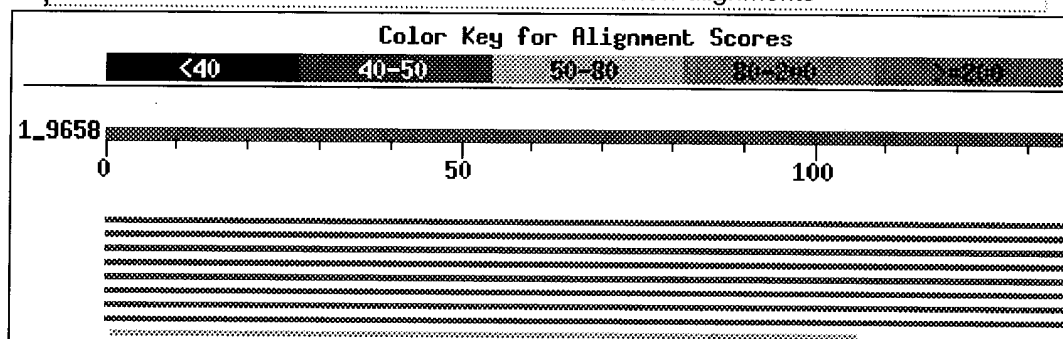
Query=

(136 letters)








**Database:** All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 1,530,482 sequences; 497,137,717 total letters

Taxonomy reports**Distribution of 355 Blast Hits on the Query Sequence**

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:	Score (bits)	E Value
<a href="#">gi 284667 pir A43427</a> neurofilament triplet H1 protein - ra...	<a href="#">334</a>	1e-90
<a href="#">gi 71549 pir QFHUH</a> neurofilament triplet H protein - human...	<a href="#">325</a>	5e-88
<a href="#">gi 32483416 ref NP_066554.2 </a> neurofilament, heavy polypepti...	<a href="#">325</a>	5e-88
<a href="#">gi 33302611 sp P12036 NFH_HUMAN</a> Neurofilament triplet H pro...	<a href="#">322</a>	3e-87
<a href="#">gi 27529742 dbj BAA74868.2 </a> KIAA0845 protein [Homo sapiens]	<a href="#">322</a>	3e-87
<a href="#">gi 601931 gb AAA57153.1 </a> neurofilament-H	<a href="#">317</a>	1e-85
<a href="#">gi 284668 pir B43427</a> neurofilament protein H form H2 (repe...	<a href="#">313</a>	2e-84
<a href="#">gi 24020878 gb AAN40837.1 AF346625_1</a> heavy neurofilament pr...	<a href="#">309</a>	3e-83
<a href="#">gi 21429606 gb AAM49796.1 </a> heavy neurofilament NF-H [Rattus...	<a href="#">271</a>	8e-72
<a href="#">gi 205686 gb AAA41695.1 </a> heavy neurofilament subunit	<a href="#">271</a>	8e-72
<a href="#">gi 14250426 gb AAH08648.1 AAH08648</a> Unknown (protein for IMA...	<a href="#">270</a>	1e-71
<a href="#">gi 128127 sp P19246 NFH_MOUSE</a> Neurofilament triplet H prote...	<a href="#">270</a>	2e-71
<a href="#">gi 28972433 dbj BAC65670.1 </a> mKIAA0845 protein [Mus musculus]	<a href="#">270</a>	2e-71
<a href="#">gi 29789026 ref NP_036739.1 </a> neurofilament, heavy polypepti...	<a href="#">268</a>	8e-71
<a href="#">gi 205680 gb AAA41692.1 </a> high molecular weight neurofilament	<a href="#">268</a>	8e-71

gi 200022 gb AAA39809.1  neurofilament protein >gi 226537 p...	267	1e-70	
gi 463250 emb CAA83229.1  Neurofilament protein, high molec...	267	1e-70	
gi 92538 pir  S02003 neurofilament triplet H protein - rat ...	245	6e-64	
gi 462702 sp P16884 NFM RAT Neurofilament triplet H protein...	245	6e-64	
gi 37549256 ref XP_291369.3  similar to KIAA0845 protein [H...	207	1e-52	
gi 13629976 sp O77788 NFM BOVIN Neurofilament triplet M pro...	152	8e-36	
gi 226213 prf  1501343A neurofilament protein NF-H C term	147	2e-34	
gi 1160355 gb AAB00542.1  UNC-89	136	4e-31	
gi 7511618 pir  T29757 protein UNC-89 - Caenorhabditis elegans	136	4e-31	
gi 31746683 gb AAP68958.1  Uncoordinated protein 89, isoform...	136	4e-31	
gi 25141314 ref NP_491290.2  UNCoordinated locomotion UNC-8...	136	4e-31	
gi 4885513 ref NP_005373.1  neurofilament 3 (150kDa medium)...	113	2e-24	
gi 6003540 gb AAF00492.1 AF181990_1 neurofilament-3 (150 kD...	111	1e-23	
gi 14149397 gb AAK54495.1 AF368231_2 neurofilament triplet ...	102	9e-21	
gi 423935 pir  A46194 neurofilament protein NF-220, high-mo...	101	1e-20	
gi 18767706 ref NP_571997.1  neurofilament triplet H1-like ...	101	2e-20	
gi 14549637 gb AAK66966.1 AF255740_1 histone H1 [Bufo bufo ...	97	2e-19	
gi 23469403 ref ZP_00124737.1  COG3064: Membrane protein in...	92	1e-17	
gi 32966575 gb AAP92164.1  histone H1 [Medicago truncatula]	92	1e-17	
gi 13540405 gb AAK29456.1 AF352253_1 histone H1 [Lens culin...	91	1e-17	
gi 13540403 gb AAK29455.1 AF352252_1 histone H1 [Lens culin...	91	1e-17	
gi 2981173 gb AAC06245.1  neurofilament medium subunit [Ser...	90	3e-17	
gi 13540395 gb AAK29451.1 AF352248_1 histone H1 [Pisum sati...	90	3e-17	
gi 128146 sp P16053 NFM CHICK Neurofilament triplet M prote...	90	3e-17	
gi 63686 emb CAA29073.1  NF-M c-terminus [Gallus gallus]	90	3e-17	
gi 7439660 pir  T06257 histone H1 (clone TH32) - wheat >gi ...	89	8e-17	
gi 21465095 gb AAM54671.1 AF514417_1 histone H1 [Pisum sati...	88	1e-16	
gi 4106696 dbj BAA36284.1  ribosome-sedimenting protein [Pi...	88	1e-16	
gi 4996567 dbj BAA78535.1  ribosome-sedimenting protein [Pi...	88	1e-16	
gi 21465093 gb AAM54670.1 AF514416_1 histone H1 [Lathyrus a...	88	2e-16	
gi 13540401 gb AAK29454.1 AF352251_1 histone H1 [Lens culin...	88	2e-16	
gi 13540391 gb AAK29449.1 AF352246_1 histone H1 [Pisum sati...	87	3e-16	
gi 13540397 gb AAK29452.1 AF352249_1 histone H1 [Lathyrus s...	87	4e-16	
gi 13540399 gb AAK29453.1 AF352250_1 histone H1 [Lathyrus s...	87	4e-16	
gi 30420974 gb AAP31307.1  histone H1 [Lens nigricans]	87	4e-16	
gi 805006 emb CAA56558.1  pprB [Pseudomonas putida]	87	4e-16	
gi 28867376 ref NP_789995.1  alginate regulatory protein Al...	85	2e-15	
gi 9630970 ref NP_047640.1  mucin-like protein [Lymantria d...	83	5e-15	
gi 13540393 gb AAK29450.1 AF352247_1 histone H1 [Pisum sati...	83	7e-15	
gi 16127671 ref NP_422235.1  arylesterase-related protein [...	82	9e-15	
gi 2114317 dbj BAA20035.1  tegument protein [Equine herpesv...	82	1e-14	
gi 5230788 gb AAD41008.1 AF107026_1 histone H1 WH1A.3 [Trit...	81	2e-14	
gi 5230790 gb AAD41009.1 AF107027_1 histone H1 WH1A.4 [Trit...	81	2e-14	
gi 7439656 pir  T06241 histone H1 (clone TH315) - wheat >gi ...	81	2e-14	
gi 30420972 gb AAP31306.1  histone H1 [Vicia hirsuta]	80	4e-14	
gi 14916992 sp P27806 H1 WHEAT Histone H1	80	4e-14	
gi 11558848 emb CAA42529.2  histone H1 [Triticum aestivum]	80	4e-14	
gi 5230781 gb AAD41005.1 AF107022_1 histone H1 WH1A.1 [Trit...	80	4e-14	
gi 5230783 gb AAD41006.1 AF107023_1 histone H1 WH1A.2 [Trit...	80	5e-14	
gi 7428714 pir  QFPGM neurofilament triplet M protein - pig...	79	7e-14	
gi 26986938 ref NP_742363.1  alginate regulatory protein Al...	79	7e-14	
gi 283442 pir  A40215 TcD antigen - Trypanosoma cruzi	79	1e-13	
gi 161958 gb AAB97874.1  surface antigen [Trypanosoma cruzi]	78	1e-13	
gi 31213063 ref XP_315475.1  ENSANGP00000021721 [Anopheles ...	78	2e-13	
gi 28209501 gb AAO37519.1  histone-like protein [Oryza sati...	77	3e-13	
gi 22963111 ref ZP_00010717.1  COG3064: Membrane protein in...	77	4e-13	
gi 283024 pir  S22322 histone H1 - wheat	74	3e-12	
gi 2118971 pir  I51227 histone H1A - African clawed frog >g...	73	4e-12	

<a href="#">gi 2623960 emb CAA73171.1 </a>	histone H1 [Apium graveolens]	72	8e-12	
<a href="#">gi 15217879 ref NP_174150.1 </a>	prolin-rich protein -related [...]	72	1e-11	
<a href="#">gi 30018740 ref NP_830371.1 </a>	Internalin protein [Bacillus c...]	71	1e-11	
<a href="#">gi 29561775 emb CAD87780.1 </a>	SI:dZ258D18.1 (novel protein si...)	71	2e-11	
<a href="#">gi 15602833 ref NP_245905.1 </a>	TolA [Pasteurella multocida] >...	71	2e-11	
<a href="#">gi 121955 sp P02254 H1_SALTR</a>	Histone H1 >gi 70667 pir  HSTR...	71	2e-11	
<a href="#">gi 2133786 pir  I51116</a>	NF-180 - sea lamprey >gi 632549 gb A...	71	2e-11	
<a href="#">gi 121922 sp P06893 H1B_XENLA</a>	HISTONE H1B >gi 2118972 pir  ...	70	5e-11	
<a href="#">gi 70670 pir  HSXL1B</a>	histone H1B - African clawed frog	70	5e-11	
<a href="#">gi 23054984 ref ZP_00081113.1 </a>	COG0532: Translation initiat...	69	6e-11	
<a href="#">gi 25143299 ref NP_492875.2 </a>	pre-mRNA splicing SR protein r...	69	6e-11	
<a href="#">gi 9626761 ref NP_041033.1 </a>	tegument protein [Equine herpes...]	69	8e-11	
<a href="#">gi 22538198 ref NP_689049.1 </a>	pathogenicity protein, putativ...	69	8e-11	
<a href="#">gi 2114319 dbj BAA20036.1 </a>	tegument protein [Equine herpesv...]	69	8e-11	
<a href="#">gi 5230785 gb AAD41007.1 AF107024.1</a>	histone H1 WH1B.1 [Trit...	68	2e-10	
<a href="#">gi 121951 sp P06350 H1_ONCMY</a>	Histone H1 [Contains: Oncorhyn...	68	2e-10	
<a href="#">gi 70668 pir  HSTR1R</a>	histone H1 - rainbow trout	68	2e-10	
<a href="#">gi 121918 sp P06892 H1A_XENLA</a>	HISTONE H1A >gi 64775 emb CAA...	67	3e-10	
<a href="#">gi 482295 pir  A36128</a>	regulatory protein algP - Pseudomonas...	67	3e-10	
<a href="#">gi 70669 pir  HSXL1A</a>	histone H1A - African clawed frog	67	3e-10	
<a href="#">gi 15600446 ref NP_253940.1 </a>	alginate regulatory protein Al...	66	5e-10	
<a href="#">gi 30420970 gb AAP31305.1 </a>	histone H1 [Vicia faba]	66	7e-10	
<a href="#">gi 4885381 ref NP_005313.1 </a>	H1 histone family, member 5 [Ho...	66	7e-10	
<a href="#">gi 25012056 ref NP_736451.1 </a>	putative peptidoglycan linked ...	66	9e-10	
<a href="#">gi 22597168 gb AAN03471.1 </a>	unknown protein [Glycine max]	66	9e-10	
<a href="#">gi 108359 pir  S02571</a>	neurofilament triplet protein H - pig...	65	1e-09	
<a href="#">gi 21426893 ref NP_064418.1 </a>	histone 1, H1b; histone 1, fam...	65	2e-09	

## Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|284667|pir||A43427](#) neurofilament triplet H1 protein - rabbit (fragment)  
[gi|601930|gb|AA57152.1|](#) neurofilament-H  
 Length = 606

Score = 334 bits (781), Expect = 1e-90

Identities = 133/189 (70%), Positives = 134/189 (70%), Gaps = 53/189 (28%)

Query: 1 AKSPAE-----AKSPAEAKSP-----AKSPAEAKSPEKAKSP--- 32  
 AKSP E AKSPAEAKSP AKSPAEAKSPEKAKSP  
 Sbjct: 39 AKSPTEGGAASPEEEAKSPAEAKSPVKEEAKSPAEAKSPAEAKSPAEAKSPEKAKSPVKE 98

Query: 33 -AKSPAEAKSPVKEEAKSP--AKSPEKAKSPAEAKSP-----AKSPEK-----A 73  
 AKSP +AKSPVKEEAKSP AKSPEKAKSPAEAKSP AKSPEK A  
 Sbjct: 99 EAKSPEKAKSPVKEEAKSPAEAKSPEKAKSPAEAKSPEKAKSPVKEEAKSPEKAKSPA EA 158

Query: 74 KSPEKAKSP--AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPAEAKSP--AKSPVKEEA 127  
 KSPEKAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSPAEAKSP AKSPVKEEA  
 Sbjct: 159 KSPEKAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPA EAKSPEKAKSPVKEEA 218

Query: 128 KSPEKAKSP 136  
 KSPEKAKSP  
 Sbjct: 219 KSPEKAKSP 227

Score = 326 bits (763), Expect = 2e-88

Identities = 132/194 (68%), Positives = 134/194 (69%), Gaps = 58/194 (29%)

Query: 1 AKSPA EAKSP-----AEAKSPA--KSPA EAKSPEKAKSP----AKSPA EAKSPVKEE 46  
AKSPA EAKSP AEAKSPA KSPA EAKSPEKAKSP AKSP +AKSPVKEE  
Sbjct: 54 AKSPA EAKSPVKEEAKSPA EAKSPA EAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPVKEE 113

Query: 47 AKSPA--KSPEKAKSPA EAKSP-----AKSPEKAKSP----- 76  
AKSPA KSPEKAKSPA EAKSP AKSPEKAKSP  
Sbjct: 114 AKSPA EAKSPEKAKSPA EAKSPA EAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPA EAKSPA EAKSPA 173

Query: 77 EKAKSP---AKSPEKAKSPVKEEAKSP-----AKSPVKEEAKSPA EAKSP--AKSP 122  
EKAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSP  
Sbjct: 174 EKAKSPVKEEAKSPEKAKSPVKEEAKSPA EAKSPA EAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPA EAKSPA 233

Query: 123 VKEEAKSPEKAKSP 136  
VKEEAKSPEKAKSP  
Sbjct: 234 VKEEAKSPEKAKSP 247

Score = 307 bits (717), Expect = 1e-82

Identities = 134/246 (54%), Positives = 134/246 (54%), Gaps = 110/246 (44%)

Query: 1 AKSPA EAKSPA-----EAKSP-----AKSPA EAKSPEKAKSP----- 32  
AKSPA EAKSP EAKSP AKSPA EAKSPEKAKSP  
Sbjct: 164 AKSPA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPA EAKSPA EAKSPA EAKSPEKAKSPVKEEAKSPEK 223

Query: 33 AKSPA EAKSPVKEEAKSP-----AKSPEKAKSP-----AEAK 64  
AKSPA EAKSPVKEEAKSP AKSPEKAKSP AEAK  
Sbjct: 224 AKSPA EAKSPVKEEAKSPEKAKSPEKEEAKSPA EAKSPA EAKSPA EAKSPEKAKSPVEVKSPA EAK 283

Query: 65 SP-----AKSPEKAKSP-----EKAKSP---AKSPEK 88  
SP AKSPEKAKSP EKAKSP AKSPEK  
Sbjct: 284 SPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 343

Query: 89 AKSPVKEEAKSP--AKSPVKEEAKSPA-----EAKSP--AKSPVKEEAKSP 130  
AKSPVKEEAKSP AKSPVKEEAKSP EAKSP AKSPVKEEAKSP  
Sbjct: 344 AKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 403

Query: 131 EKAKSP 136  
EKAKSP  
Sbjct: 404 EKAKSP 409

Score = 240 bits (559), Expect = 2e-62

Identities = 117/238 (49%), Positives = 120/238 (50%), Gaps = 104/238 (43%)

Query: 1 AKSPA EAKSPA EAKSP--AKSPA--EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP-- 50  
AKSP E KSPA EAKSP AKSP EAKSPEKAKSP AKSP +AKSPVKEEAKSP  
Sbjct: 270 AKSPVEVKSPA EAKSPA EAKSPA EAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 329

Query: 51 -----AKSPEKAKSPA--EAKSP-----AKSPEKAKSPEKAKSP----- 82  
AKSPEKAKSP EAKSP AKSPEKAKSPEKAKSP  
Sbjct: 330 AKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSP 389

Query: 83 -----AKSPEKAKSPVKEEAKSPA K-SPVKEEAK----- 110



EKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAKSPEKAK  
Sbjct: 692 EKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAK 751

Query: 135 SP 136  
SP  
Sbjct: 752 SP 753

Score = 316 bits (738), Expect = 3e-85  
Identities = 131/202 (64%), Positives = 132/202 (65%), Gaps = 66/202 (32%)

Query: 1 AKSPA-----AKSPA-----AKSPA 22  
AKSPA AKSP EAKSP AKSPA  
Sbjct: 538 AKSPA EVKSPEKAKSPA EEA KSPPEAKSPEKEEAKSPA EVKSPEKAKSPA EEA KSPA 597

Query: 23 AKSPEKAKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72  
AKSPEKAKSP AKSPA EAKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK  
Sbjct: 598 AKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEK 657

Query: 73 --AKSPEKAKSP----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116  
AKSPEKAKSP AKSPEKAKSPV EAKSP AKSPVKEEAKSP EAK  
Sbjct: 658 EEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAK 717

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136  
SP AKSPVKEEAK+PEKAKSP  
Sbjct: 718 SPEKAKSPVKEEAKTPEKAKSP 739

Score = 309 bits (723), Expect = 3e-83  
Identities = 130/196 (66%), Positives = 130/196 (66%), Gaps = 60/196 (30%)

Query: 1 AKSPA--EAKSPA EAKSP----AKSPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50  
AKSP EAKSPA EAKSP AKSPA KSPEKAKSP AKSP EAKSP KEEAKSP  
Sbjct: 516 AKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA EEA KSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76  
A KSPEKAKSPA EAKSP AKSPEKA KSP  
Sbjct: 576 AEVKSPEKAKSPA EEA KSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSP 635

Query: 77 EKAKSP----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAKSP--AK 120  
EKAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAKSP AK  
Sbjct: 636 EKAKSPTKEEAKSPEKAKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAK 695

Query: 121 SPVKEEAKSPEKAKSP 136  
SPVKEEAKSPEKAKSP  
Sbjct: 696 SPVKEEAKSPEKAKSP 711

Score = 280 bits (653), Expect = 2e-74  
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPA KSPA E--AKSPEK--AKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA-- 61  
E KSP PAE A SPEK AKSP AKSPA EAKSP KEEAKSPA KSPEKAKSPA  
Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA E 556

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP-- 100  
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP

Sbjct: 557 EAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPA EAKSP--AKSPVKEEAKSPEKAKSP 136  
AKSPVKEEAKSPA E KSP AKSP KEEAKSPEKAKSP

Sbjct: 617 EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSP 655

Score = 261 bits (608), Expect = 1e-68

Identities = 121/235 (51%), Positives = 124/235 (52%), Gaps = 99/235 (42%)

Query: 1 AKSPA--EAKSPA EAKSP----AKSPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50  
AKSP EAKSPA EAKSP AKSPA E KSPEKAKSP AKSP +AKSP KEEAKSP  
Sbjct: 604 AKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEKEEAKSP 663

Query: 51 -----AKSPEKAKSP--AEAKSP-----AKSPEKAKSP-----EKAK 80  
AKSPEKAKSP AEAKSP AKSPEKAKSP EKAK  
Sbjct: 664 EKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAK 723

Query: 81 SP----AKSPEKAKSPVKEEAKSP----- 100  
SP AK+PEKAKSPVKEEAKSP  
Sbjct: 724 SPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARS PADKFPE 783

Query: 101 -AKSPVKEEAKSPA EAKSP-----AKSPVKEEAKSPE-KAKSP 136  
AKSPVKEE KSP +AKSP KSPVKEE K E K K P  
Sbjct: 784 KAKSPVKEEVKSPEKAKSPLKADAKAPEKEIPKKEEVKSPVKEEEKPQEVKVKEP 838

Score = 210 bits (488), Expect = 3e-53

Identities = 117/272 (43%), Positives = 124/272 (45%), Gaps = 139/272 (51%)

Query: 1 AKSPA EAKSP--AEAKSP--AKSP--AEAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50  
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP  
Sbjct: 660 AKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 719

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAK-----SPEKAKSPA K-----SP- 86  
AK+PEKAKSP EAKSP AKSPEKAK SPE AK+PAK SP  
Sbjct: 720 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPE-AKTPAKEEARS PA 778

Query: 87 -----EKAKSPVKEE-----AKSP-----AKSPVKE----- 107  
EKAKSPVKEE AKSP KSPVKE  
Sbjct: 779 DKFPEKAKSPVKEEVKSPEKAKSPLKADAKAPEKEIPKKEEVKSPVKEEEKPQEVKVKEP 838

Query: 108 -----EAKSPA-----EAK----- 116  
E K+PA EAK  
Sbjct: 839 PKKAE E EKAPATPKTEEKKDSKKEEAPKKEAPKPKVKEEKKEPAVEKPKESKVEAKKEEAE 898

Query: 117 -----SPA KSPVKEEAKSPEK---AK 134  
+PAK VKE+AK EK AK  
Sbjct: 899 DKKKVPTPEKEAPAKVEVKEDAKPKTEKTEVAK 930

Score = 100 bits (229), Expect = 3e-20

Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPA EAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP----AKSPA-----EA 39  
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E  
Sbjct: 762 KSP-EAKTPAKEEARS PADKFPEKAKSPVKEEVKSPEKAKSPLKADAKAPEKEIPKKEEV 820

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60  
 KSPVKE E K+PA K+ EK A K P  
 Sbjct: 821 KSPVKEEEKPQEVKVKEPPKAAEEKAPATPKTEEEKDKSKKEEAPKKEAPKPKVEEEKKEP 880



Query: 61 A-----EAK-----SPAK-----SP-EKA-----KSPE--KAKS 81  
 A EAK +PAK P EK K P+ KAK  
 Sbjct: 881 AVEKPKESKVEAKKEEAEDKKKVPTPEKEAPAKVEVKEDAKPKTEVAKKEPDDAKAKE 940

Query: 82 PAKSPEKAKSPVKEEAKSPAKSPVKEE-AKSPA-EAKSPAKSPVKEEAKS----P----- 130  
 P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P  
 Sbjct: 941 PSKPAEK-----KEAA--PEKKDTKEEKAKKPPEEKPKTEAKA--KEDDKTLSKEPSKPKA 991

Query: 131 EKA-KS 135  
 EKA KS  
 Sbjct: 992 EKAES 997

Score = 97.8 bits (223), Expect = 2e-19  
 Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPA-EAKSP---AKSPVKEEAKSPEKAKSP 136  
 E+ KSP EEA SP AKSPVKEEAKSPA-EAKSP AKSP E KSPEKAKSP  
 Sbjct: 499 EETKSPPAEEAASPEKEAKSPVKEEAKSPA-EAKSPEKEEAKSP--AEVKSPEKAKSP 553

 >gi|32483416|ref|NP\_066554.2|  neurofilament, heavy polypeptide 200kDa; Neurofi  
 polypeptide; neurofilament, heavy polypeptide (200kD)  
 [Homo sapiens]  
 Length = 1020

Score = 325 bits (760), Expect = 5e-88  
 Identities = 130/182 (71%), Positives = 132/182 (72%), Gaps = 46/182 (25%)

Query: 1 AKSPA-EAKSPA-EAKSPA-----SPA-EAKSPEKAKSP-----AKSPA-EAKSPVKEEAKSPA- 51  
 AKSPA-E KSP +AKSPA SPA-EAKSPEKAKSP AKSPA-EAKSPVKEEAKSPA  
 Sbjct: 572 AKSPA-EVKSPEKAKSPA-E-EAKSPA-EAKSPEKAKSPVKEEAKSPA-EAKSPVKEEAKSPA-E 631

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EAKSP-----AKSP 86  
 KSPEKAKSP EAKSP AKSPEKAKSP EAKSP AKSP  
 Sbjct: 632 VKSPEKAKSP-TKEEAKSPEKAKSPEKEEAKSPEKAKSPVKA-EAKSPEKAKSPVKA-EAKSP 691

Query: 87 EKAKSPVKEEAKSP--AKSPVKEEAKSPA-EAKSP-----AKSPVKEEAKSPEKAK 134  
 EKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAKSPEKAK  
 Sbjct: 692 EKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAK 751

Query: 135 SP 136  
 SP  
 Sbjct: 752 SP 753

Score = 316 bits (738), Expect = 3e-85  
 Identities = 131/202 (64%), Positives = 132/202 (65%), Gaps = 66/202 (32%)

Query: 1 AKSPA-E-----AKSPA-EAKSP-----AKSPA-E 22  
 AKSPA-E AKSP EAKSP AKSPA-E  
 Sbjct: 538 AKSPA-EVKSPEKAKSPA-E-EAKSPA-E-EAKSPA-EVKSPEKAKSPA-E-EAKSPA-E 597

Query: 23 AKSPEKAKSP----AKSPAEAKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72  
AKSPEKAKSP AKSPAEAKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK  
Sbjct: 598 AKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEK 657

Query: 73 --AKSPEKAKSP----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116  
AKSPEKAKSP AKSPEKAKSPVK EAKSP AKSPVKEEAKSP EAK  
Sbjct: 658 EEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAK 717

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136  
SP AKSPVKEEAK+PEKAKSP  
Sbjct: 718 SPEKAKSPVKEEAKTPEKAKSP 739

Score = 309 bits (723), Expect = 3e-83  
Identities = 130/196 (66%), Positives = 130/196 (66%), Gaps = 60/196 (30%)

Query: 1 AKSPA--EAKSPAEAKSP----AKSPAEAKSPEKAKSP----AKSPAEAKSPVKEEAKSP 50  
AKSP EAKSPAEAKSP AKSPA EKSPEKAKSP AKSP EAKSP KEEAKSP  
Sbjct: 516 AKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76  
A KSPEKAKSPA EAKSP AKSPEKA KSP  
Sbjct: 576 AEVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSP 635

Query: 77 EKAKSP----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAKSP--AK 120  
EKAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAKSP AK  
Sbjct: 636 EKAKSPTKEEAKSPEKAKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAK 695

Query: 121 SPVKEEAKSPEKAKSP 136  
SPVKEEAKSPEKAKSP  
Sbjct: 696 SPVKEEAKSPEKAKSP 711

Score = 280 bits (653), Expect = 2e-74  
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPA KSPA E--AKSPEK--AKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA-- 61  
E KSP PAE A SPEK AKSP AKSPA EAKSP KEEAKSPA KSPEKAKSPA  
Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KE 556

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP- 100  
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP  
Sbjct: 557 EAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPA EAKSP--AKSPVKEEAKSPEKAKSP 136  
AKSPVKEEAKSPA E KSP AKSP KEEAKSPEKAKSP  
Sbjct: 617 EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSP 655

Score = 228 bits (531), Expect = 8e-59  
Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPA EAKSP--AEAKSP--AKSP--AEAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50  
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP  
Sbjct: 660 AKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 719

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAKS----- 75  
AK+PEKAKSP EAKSP AKSPEKAK+  
Sbjct: 720 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARSPAD 779

Query: 76 --PEKAKSPAK----SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPA EAKSPAK 120  
PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K  
Sbjct: 780 KFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPVKEEEK-PQEVK---- 834

Query: 121 SPVKEEAKSPEKAKSP 136  
VKE K E+ K+P  
Sbjct: 835 --VKEPPKKA EEEKAP 848

Score = 100 bits (229), Expect = 3e-20  
Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPA EAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP----AKSPA-----EA 39  
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E  
Sbjct: 762 KSP-EAKTPAKEEARSPADKFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEV 820

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60  
KSPVKE E K+PA K+ EK A K P  
Sbjct: 821 KSPVKEEEKPQEVKVKEPPKKA EEEKAPATPKTEEEKDSKKEEAPKKEAPKPKVEEKKEP 880




Query: 61 A-----EAK-----SPAK-----SP-EKA----KSPE--KAKS 81  
A EAK +PAK P EK K P+ KAK  
Sbjct: 881 AVEKPKESKVEAKKEEAEDKKKVPTPEKEAPAKVEVKEDAKPKEKTEVAKKEPDDAKAKE 940

Query: 82 PAKSPEKAKSPVKEEAKSPA KSPVKEE-AKSPA E-AKSPA KSPVKEEAKS-----P----- 130  
P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P  
Sbjct: 941 PSKPAEK-----KEAA--PEKKDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 991

Query: 131 EKA-KS 135  
EKA KS  
Sbjct: 992 EKA EKS 997

Score = 97.8 bits (223), Expect = 2e-19  
Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPA EAKSP---AKSPVKEEAKSPEKAKSP 136  
E+ KSP EEA SP AKSPVKEEAKSPA EAKSP AKSP E KSPEKAKSP  
Sbjct: 499 EETKSPPAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSP--AEVKSPEKAKSP 553

 >gi|33302611|sp|P12036|NFH HUMAN  Neurofilament triplet H protein (200 kDa neur  
(Neurofilament heavy polypeptide) (NF-H)  
gi|6470331|gb|AAF13722.1|AF203032.1  neurofilament protein [Homo sapiens]  
Length = 1026

Score = 322 bits (754), Expect = 3e-87  
Identities = 130/188 (69%), Positives = 132/188 (70%), Gaps = 52/188 (27%)

Query: 1 AKSPA EAKSPA EAKSPA KSP+AKSPA SPA EAKSPEKAKSP AKSPA EAKSPVKEEAKSPA 51  
AKSPA EAKSPA EAKSPA KSP+AKSPA SPA EAKSPEKAKSP AKSPA EAKSPVKEEAKSPA  
Sbjct: 572 AKSPA EVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA E 631

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EKAKSP-- 82  
KSPEKAKSP EAKSP AKSPEKAKSP EKAKSP  
Sbjct: 632 VKSPEKAKSPTKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKAEAKSPEKAKSPVK 691

Query: 83 --AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPA EAKSP-----AKSPVKEEAK 128  
AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAK  
Sbjct: 692 AEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAK 751

Query: 129 SPEKAKSP 136  
SPEKAKSP  
Sbjct: 752 SPEKAKSP 759

Score = 313 bits (732), Expect = 2e-84  
Identities = 131/208 (62%), Positives = 132/208 (63%), Gaps = 72/208 (34%)

Query: 1 AKSPA E-----AKSPA EAKSP-----AKSPA 22  
AKSPA AKSP EAKSP AKSPA  
Sbjct: 538 AKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA 597

Query: 23 AKSPEKAKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72  
AKSPEKAKSP AKSPA EAKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK  
Sbjct: 598 AKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEK 657

Query: 73 AKSPEK--AKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP----- 112  
AKSPEK AKSP AKSPEKAKSPVK EAKSP AKSPVKEEAKSP  
Sbjct: 658 AKSPEKEEAKSPEKAKSPVKAEAKSPEKAKSPVKAEAKSPEKAKSPVKEEAKSPEKAKSP 717

Query: 113 --AEAKSP--AKSPVKEEAKSPEKAKSP 136  
EAKSP AKSPVKEEAK+PEKAKSP  
Sbjct: 718 VKEEAKSPEKAKSPVKEEAKTPEKAKSP 745

Score = 307 bits (717), Expect = 1e-82  
Identities = 130/202 (64%), Positives = 130/202 (64%), Gaps = 66/202 (32%)

Query: 1 AKSPA--EAKSPA EAKSP----AKSPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50  
AKSP EAKSPA EAKSP AKSPA KSPEKAKSP AKSP EAKSP KEEAKSP  
Sbjct: 516 AKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76  
A KSPEKAKSPA EAKSP AKSPEKA KSP  
Sbjct: 576 AEVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSP 635

Query: 77 EKAKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116  
EKAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAK  
Sbjct: 636 EKAKSPTKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKAEAKSPEKAKSPVKAEAK 695

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136  
SP AKSPVKEEAKSPEKAKSP  
Sbjct: 696 SPEKAKSPVKEEAKSPEKAKSP 717

Score = 280 bits (653), Expect = 2e-74  
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPAKSPAE-AKSPEK-AKSP----AKSPAEAKSPVKEEAKSPA--KSPEKAKSPA-- 61  
E KSP PAE A SPEK AKSP AKSPAEAKSP KEEAKSPA KSPEKAKSPA  
Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPAEAKSPEKEEAKSPAENVKSPEKAKSPA 556

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP- 100  
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP  
Sbjct: 557 EAKSPPEAKSPEKEEAKSPAENVKSPEKAKSPAEEAKSPAEEAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPAEAKSP--AKSPVKEEAKSPEKAKSP 136  
AKSPVKEEAKSPA KSP AKSP KEEAKSPEKAKSP  
Sbjct: 617 EAKSPVKEEAKSPAENVKSPEKAKSPTEKEEAKSPEKAKSP 655

Score = 228 bits (531), Expect = 8e-59

Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPAEAKSP--AEAKSP--AKSP--AEAKSPEKAKSP----AKSPAEAKSPVKEEAKSP 50  
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP  
Sbjct: 666 AKSPEKAKSPVKAEEAKSPEKAKSPVKAEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 725

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAKS----- 75  
AK+PEKAKSP EAKSP AKSPEKAK+  
Sbjct: 726 EAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARS PAD 785

Query: 76 --PEKAKSPAK----SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPAEEAKSPAK 120  
PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K  
Sbjct: 786 KFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPVKEEEK-PQEVK---- 840

Query: 121 SPVKEEAKSPEKAKSP 136  
VKE K E+ K+P  
Sbjct: 841 --VKEPPKAEEEKAP 854

Score = 100 bits (229), Expect = 3e-20

Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPAEAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP----AKSPA-----EA 39  
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E  
Sbjct: 768 KSP-EAKTPAKEEARS PADKFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEV 826

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60  
KSPVKE. E K+PA K+ EK A K P  
Sbjct: 827 KSPVKEEEKPQEVKVKEPPKAEEEKAPATPKTEEEKKDSKKEEAPKKEAPKPKVEEEKKEP 886

Query: 61 A-----EAK-----SPAK-----SP-EKA----KSPE--KAKS 81  
A EAK +PAK P EK K P+ KAK  
Sbjct: 887 AVEKPKESKVEAKKEEAEDKKKVPTPEKEAPAKVEVKEDAKPKEKTEVAKKEPDDAKAKE 946

Query: 82 PAKSPEKAKSPVKEEAKSPA KSPVKEE-AKSPA E-AKSPA KSPVKEEAKS-----P----- 130  
P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P  
Sbjct: 947 PSKPAEK-----KEAA--PEKKDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 997

Query: 131 EKA-KS 135  
EKA KS  
Sbjct: 998 EKA EKS 1003

Score = 97.8 bits (223), Expect = 2e-19  
Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPA EAKSP---AKSPVKEEAKSPEKAKSP 136  
E+ KSP EEA SP AKSPVKEEAKSPA EAKSP AKSP E KSPEKAKSP  
Sbjct: 499 EETKSPPAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSP--AEVKSPEKAKSP 553

 >gi|27529742|dbj|BAA74868.2|  KIAA0845 protein [Homo sapiens]  
Length = 1034

Score = 322 bits (754), Expect = 3e-87  
Identities = 130/188 (69%), Positives = 132/188 (70%), Gaps = 52/188 (27%)

Query: 1 AKSPA EAKSPA EAKSPA K----SPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSPA- 51  
AKSPA E KSP +AKSPA K SPA EAKSPEKAKSP AKSPA EAKSPVKEEAKSPA  
Sbjct: 580 AKSPA EVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA E 639

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EKAKSP-- 82  
KSPEKAKSP EAKSP AKSPEKAKSP EKAKSP  
Sbjct: 640 VKSPEKAKSPTKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVK 699

Query: 83 --AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPA EAKSP-----AKSPVKEEAK 128  
AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAK  
Sbjct: 700 AEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAK 759

Query: 129 SPEKAKSP 136  
SPEKAKSP  
Sbjct: 760 SPEKAKSP 767

Score = 313 bits (732), Expect = 2e-84  
Identities = 131/208 (62%), Positives = 132/208 (63%), Gaps = 72/208 (34%)

Query: 1 AKSPA E-----AKSPA EAKSP-----AKSPA E 22  
AKSPA E AKSP EAKSP AKSPA E  
Sbjct: 546 AKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA E 605

Query: 23 AKSPEKAKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72  
AKSPEKAKSP AKSPA EAKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK  
Sbjct: 606 AKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEK 665

Query: 73 AKSPEK--AKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP----- 112  
AKSPEK AKSP AKSPEKAKSPVK EAKSP AKSPVKEEAKSP  
Sbjct: 666 AKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSP 725

Query: 113 --AEAKSP--AKSPVKEEAKSPEKAKSP 136  
EAKSP AKSPVKEEAK+PEKAKSP  
Sbjct: 726 VKEEAKSPEKAKSPVKEEAKTPEKAKSP 753

Score = 307 bits (717), Expect = 1e-82  
Identities = 130/202 (64%), Positives = 130/202 (64%), Gaps = 66/202 (32%)

Query: 1 AKSPA--EAKSPA EAKSP----AKSPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50  
AKSP EAKSPA EAKSP AKSPA E KSPEKAKSP AKSP EAKSP KEEAKSP  
Sbjct: 524 AKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSP 583

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76  
A KSPEKAKSPA EAKSP AKSPEKA KSP  
Sbjct: 584 AEVKSPEKAKSPAKEEAKSPA EAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSP 643

Query: 77 EAKAKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116  
EAKAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAK  
Sbjct: 644 EAKAKSPTKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAK 703

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136  
SP AKSPVKEEAKSPEKAKSP  
Sbjct: 704 SPEKAKSPVKEEAKSPEKAKSP 725

Score = 280 bits (653), Expect = 2e-74  
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPA KSPA E--AKSPEK--AKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA-- 61  
E KSP PAE A SPEK AKSP AKSPA EAKSP KEEAKSPA KSPEKAKSPA  
Sbjct: 508 ETKSP---PAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSP EAKSPA E 564

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP-- 100  
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP  
Sbjct: 565 EAKSPPEAKSPEKEEAKSPA EVKSP EAKSPA EAKSPEKAKSPVKEEAKSPA 624

Query: 101 -AKSPVKEEAKSPA EAKSP--AKSPVKEEAKSPEKAKSP 136  
AKSPVKEEAKSPA E KSP AKSP KEEAKSPEKAKSP  
Sbjct: 625 EAKSPVKEEAKSPA EVKSP EAKSPA EAKSPTKEEAKSPEKAKSP 663

Score = 228 bits (531), Expect = 8e-59  
Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPA EAKSP--AEAKSP--AKSP--AEAKSPEKAKSP-----AKSPA EAKSPVKEEAKSP 50  
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP  
Sbjct: 674 AKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 733

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAKS----- 75  
AK+PEKAKSP EAKSP AKSPEKAK+  
Sbjct: 734 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARS PAD 793

Query: 76 --PEKAKSPAK----SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPA EAKSPAK 120  
PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K  
Sbjct: 794 KFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPVKEEEK-PQEVK---- 848

Query: 121 SPVKEEAKSPEKAKSP 136  
VKE K E+ K+P  
Sbjct: 849 --VKEPPKAE E E E KAP 862

Score = 100 bits (229), Expect = 3e-20  
Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPA EAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP-----AKSPA-----EA 39  
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E  
Sbjct: 776 KSP-EAKTPAKEEARS PADKFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEV 834

Score = 97.8 bits (223), Expect = 2e-19  
Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

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>gi|601931|qb|AAA57153.1| neurofilament-H
Length = 511
```

Score = 317 bits (741), Expect = 1e-85  
Identities = 127/172 (73%), Positives = 130/172 (75%), Gaps = 36/172 (20%)

Query: 95 EEA KSP-----AKSPVKEEA KSPA EAKSP--AKSPVKEEA KSPEKA KSP 136  
 EEA KSP AKSPVKEEA KSP +AKSP AKSPVKEEA KSPEKA KSP  
 Sbjct: 314 EEA KSPEKA KSPEKA KSPVKEEA KSPEKA KSPEKA KSPVKEEA KSPEKA KSP 365

Score = 312 bits (729), Expect = 4e-84  
Identities = 132/219 (60%), Positives = 132/219 (60%), Gaps = 84/219 (38%)

Query: 77 -----EKAKSP-----AKSPEKAKSPVKEEAKSP-----AKSPVKEEAKSP----- 112  
 EKAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP